cDNA Sequence of human IBR

Two alternativ 5' ends:

1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA
2 AAGGAAGGAGGGAGAAGGGAAGGAGTGAAGGAAGGAGTGAAA

Common Sequence:

AGGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA 60
TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC 120
TGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGG 180
ATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG 240
GGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300
GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACCTCCAGCT 360
TCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG 420
TCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACT 480
TCCAGCAGTGTGACTAGGGCAACGTGCCCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGG 540
GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTTCTGCTCTCAGGACCCC 600
CAGGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCCAGTTTGCATAAATT 660
CTGAGATTTGGAGCTCAGTCCAGGGTCCTCCCCCACTGGATGGTGCTACTGCTGTGGAAC 720
CTTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGG 780
GTGGGGGAGTGCTGGGAATCATTCCTGCTTAATGGTAACTGACAAGTGTTACCCTGAGCC 840
CCGCAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 900
CTCTCACTCACCACTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCT 960
TGGCCCAGCCCCACCCCCTTCCCTTTATCCTGCCACTGTCATATGCTACCTTTCCTATCT 1020
CTTCCCTCATCATCTTGTTGTGGCATGAGGAGGTGGTGATGTCAGAAGAAATGGTTCGA 1080
GCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAAGATACAA 1140
TCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAG 1200
ACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAATTAAAAGATACCTATTTATAT 1260
ATTTCTTTATAGAAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGT 1320
GGCAGTATAGGTGATTTTTCTTTTAATTCTGTTAATTTATCTGTATTTCCTAATTTTTCT 1380
ACAATGAAGATGAATTCCTTGTATAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAG 1440

Fig. 1

AGCAGACATCATCTCTGATTGTCCTCAGCCTCCAATTCCCCAGAGTAAATTCAAATTGAA 1500

TCGAGCTCTGCTGCTCTGGTTGGTTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCC 1560

ACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAGGAACTTAAAG 1620

AACAAAAATCATCTGGTAATTCTTTCCTAGAAGGATCACAGCCCCTGGGATTCCAAGGCA 1680

TTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTCAC 1740

ATCCTTCTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAGT 1800

TAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCAATATGACTGGTTTCCT 1860

TGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTAAAGATGA 1920

AGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACCAT 1980

CAGAAGCTTGGAAGAGGCAAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCT 2040

CTGCTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTCGGC 2100

TGTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCTA 2160

AAATGATCCCTGTCTCCTCGTGTTTACATTCTGTGTGTGTCCCCTCCCACAATGTACCAA 2220

AGTTGTCTTTGTGACCCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTA 2280

GGTTATAAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCC 2340

AATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCTAT 2400

AAAGAGACTTACGTGGTAAAAAATGAAGTCTCCTGCCCACAGCCACATTAGTGAACCTAG 2460

AAGCAGAGACTCTGTGAGATAATCGATGTTTGTTGTTTTAAGTTGCTCAGTTTTGGTCTA 2520

ACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG(A_n) 2562

Fig. 1 (Continued)

cDNA Sequence of murine IBR

```
GGCACGAGGGGAGCCTGCTTTCTACTTAGGTCTCAAATTTTCCAGCCTTGTCTTTGCCTA     60
AAATTTCCTGCTGTTTATTTCAAAATAGGGTCTACATACTGTGGAGCTCATGATGGTTCT    120
GAGTGGGGCACTATGCTTCCGAATGAAGGATTCAGCCTTGAAGGTACTGTATCTGCACAA    180
TAACCAGCTGCTGGCTGGAGGACTGCACGCAGAGAAGGTCATTAAAGGTGAGGAGATCAG    240
TGTTGTCCCAAATCGGGCACTGGATGCCAGTCTGTCCCCTGTCATCCTGGGCGTTCAAGG    300
AGGAAGCCAGTGCCTATCTTGTGGGACAGAGAAAGGCCAATTCTGAAACTTGAGCCAGT    360
GAACATCATGGAGCTCTACCTCGGGGCCAAGGAATCAAAGAGCTTCACCTTCTACCGGCG    420
GGATATGGGTCTTACCTCCAGCTTCGAATCCGCTGCCTACCCAGGCTGGTTCCTCTGCAC    480
CTCACCGGAAGCTGACCAGCCTGTCAGGCTCACTCAGATCCCTGAGGACCCCGCCTGGGA    540
TGCTCCCATCACAGACTTCTACTTTCAGCAGTGTGACTAGGGCTGCGTGGTCCCCAAAAC    600
TCCATAAGCAGAGGCAGAGTAGGCAGTGGCGGCTCCTGATAGAGGATAGAGAGACAGAGG    660
AGCTCCACAGTAGGTGGCTTACTCCTCTCCTTCCCTACTGGACTCCCGCTTCTGACCTAA    720
GGCACACAGACACTCTCTTCTCCTGCATCCCAGTGCTGGTAAATCTTCTGGTATTTGGAG    780
CTCAATGTGTAGATTCTTTCAGATTGGATGGTACTACCTCTGGTGTGGAACCCAATAGAA    840
ACCACGTAGGACCAACAAAGAGCAACATAAAAGATTCTTGGGTGAAGAAGAGGTGGGAAC    900
TGTTCATACATAGTAAGATCTGACACAGTACCTCAGAAGTCCTGCCATTCCTTATGTTCT    960
GGAGAAAGTGGAGGGGGGGTCACCAAGACTTTCTCTGGCTGGCTGGGCCCTTTCCCTCAA   1020
CCTTTCTGACATCTGCAGCCTCTCTCATTCTTGCCTTCATTCTCTGGCCCTGAACCGAGA   1080
GGGTGATATCAGGATAGCTGACAGAAGATGACCAGGCACACTGTCCTGGTTTGAAACCAG   1140
AGGGGACAATAAAAAACCCTGATTCTGGTCTCTACTCACATAAAAAGAAGCTTGTGAACA   1200
TTAAGTGGGAAGAGATTGCTACTAAATAACATACCTTGTAATTTCATCTTAATTAAAATA   1260
TACTTCTCTATATTATATATTTTA(n)                                    1284
```

Fig. 2

Human IBR polypeptide

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

Fig. 3A

Mouse IBR polypeptide

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAEKVIKGE EISVVPNRAL
DASLSPVILG VQGGSQCLSC GTEKGPILKL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTSPEADQP VRLTQIPEDP AWDAPITDFY
FQQCD

Fig. 3B

Comparison of Human and Mouse IBR Polypeptide Sequences

```
mIBR: 1   MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEEISVVPNRALDASLSPVILG 60
          MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHA KVIKGEEISVVPNR-LDASLSPVILG IBRcon.
hIBR: 1   MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILG 60

mIBR: 61  VQGGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF 120
          VQGGSQCLSCG--+-P+L-LEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF IBRcon.
hIBR: 61  VQGGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF 120

mIBR: 121 LCTSPEADQPVRLTQIPEDPAWDAPITDFYFQQCD 155
          LCT-PEADQPVRLTQ+PE+--W+APITDFYFQQCD IBRcon.
hIBR: 121 LCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD 155
```

Fig. 4

RECEIVED
SEP 19 2002
TECH CENTER 1600/2900

Comparison of Human IBR and pro-IL-Ira Polypeptide Sequences

```
hIL-lra:  38 FRIWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVP-------IEPHALFLGIHGGKM 90
             FR+ D   K  YL NNQL+AG L      V   E+I VVP       + P  + LG+ GG   con.
hIBR    :  9 FRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSP--VILGVQGGSQ 66

hIL-lra:  91 CLSCVRSGDETKLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAM 150
             CLSC    G E  L LE VNI +L      K+ K F F R D G T+SFESAA PGWFLCT   con.
hIBR    : 67 CLSC-GVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVP 125

hIL-lra: 151 EADQPVSLTNMPDEG---VMVTKFYFQE 175
             EADQPV LT +P+ G     +T FYFQ+ con.
hIBR    : 126 EADQPVRLTQLPENGGWNAPITDFYFQQ 153
```

Fig. 5

Recombinant IBR Polypeptides

```
MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

 VLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

GSSVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
  DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
  YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
  FQQCD
```

Fig. 6

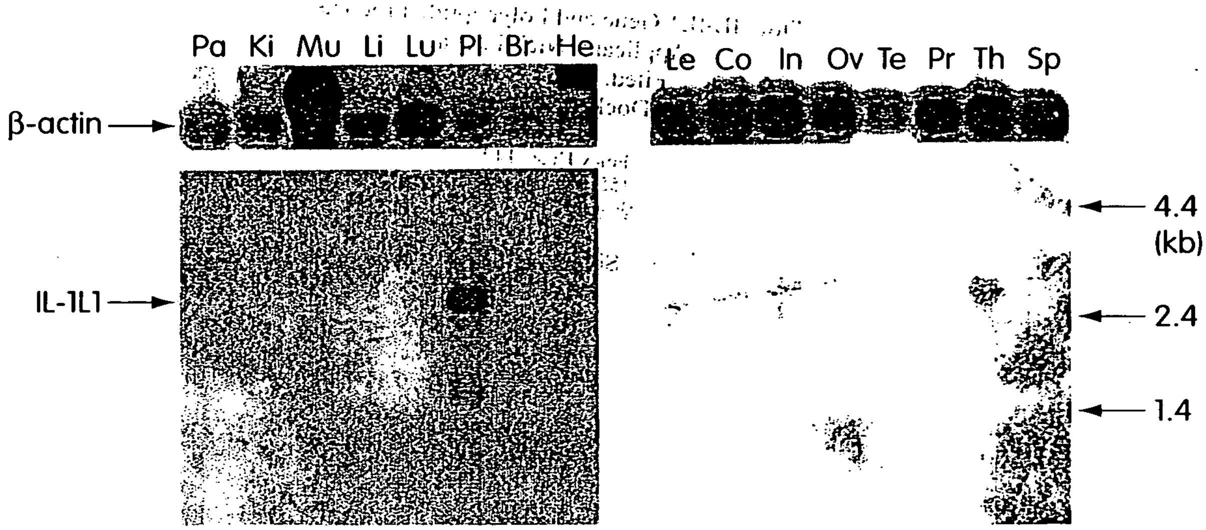
Pa
Ki
Mu
Li
Lu
Pl
Br
He
Le
Co
In
Ov
Te
Pr
Th
Sp
β-actin
IL-1L1
4.4
(kb)
2.4
1.4

Fig. 7A

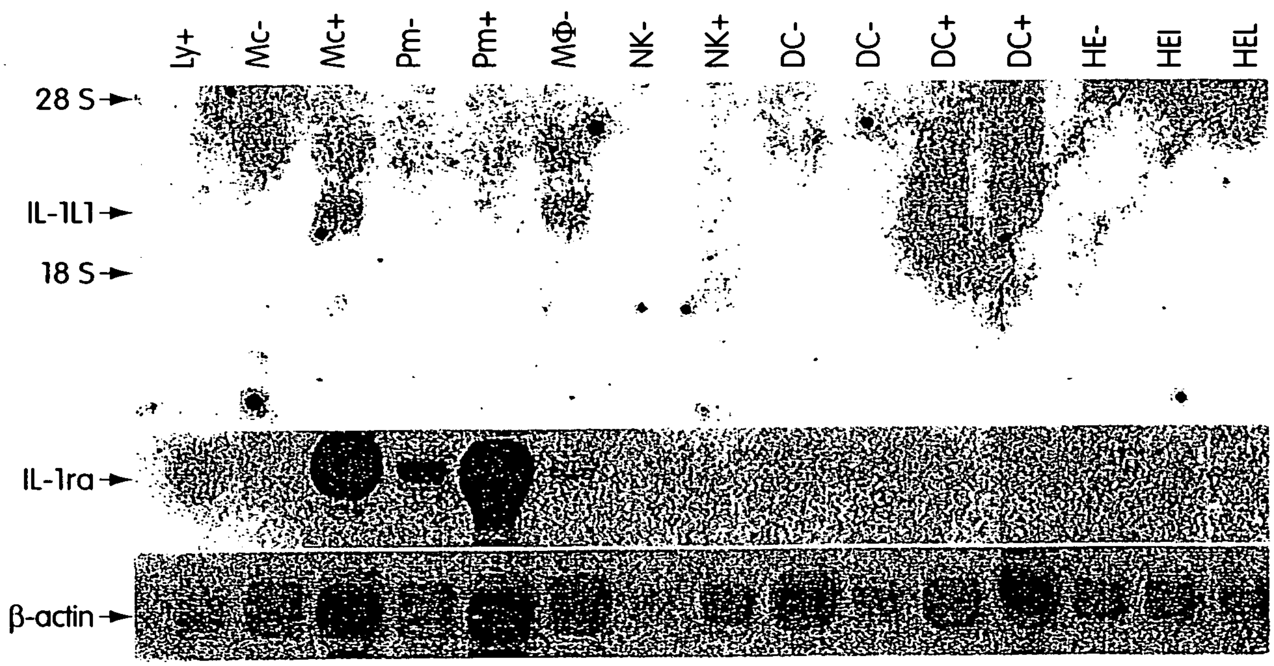
Ly+
Mc-
Mc+
Pm-
Pm+
MΦ-
NK-
NK+
DC-
DC-
DC+
DC+
HE-
HEI
HEL
28 S
IL-1L1
18 S
IL-1ra
β-actin

Fig. 7B

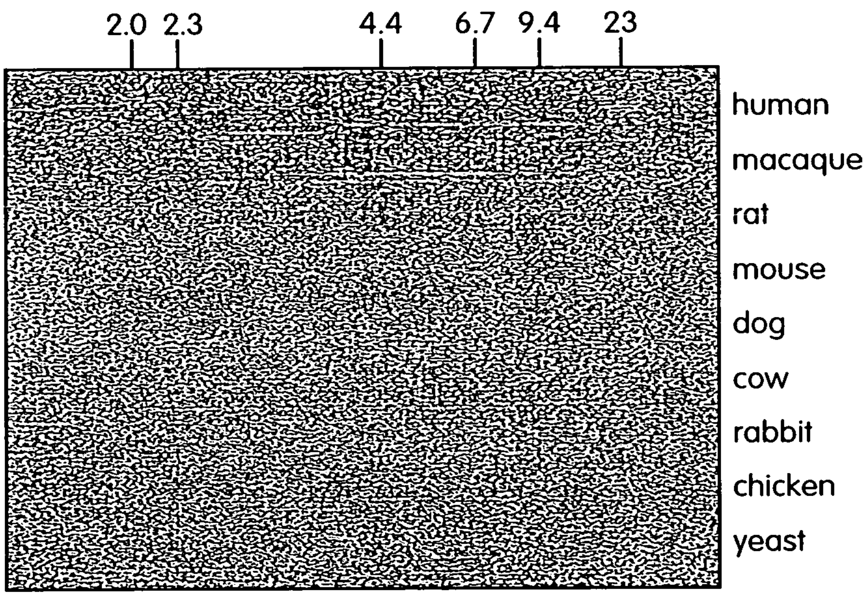
2.0
2.3
4.4
6.7
9.4
23
human
macaque
rat
mouse
dog
cow
rabbit
chicken
yeast

Fig. 8

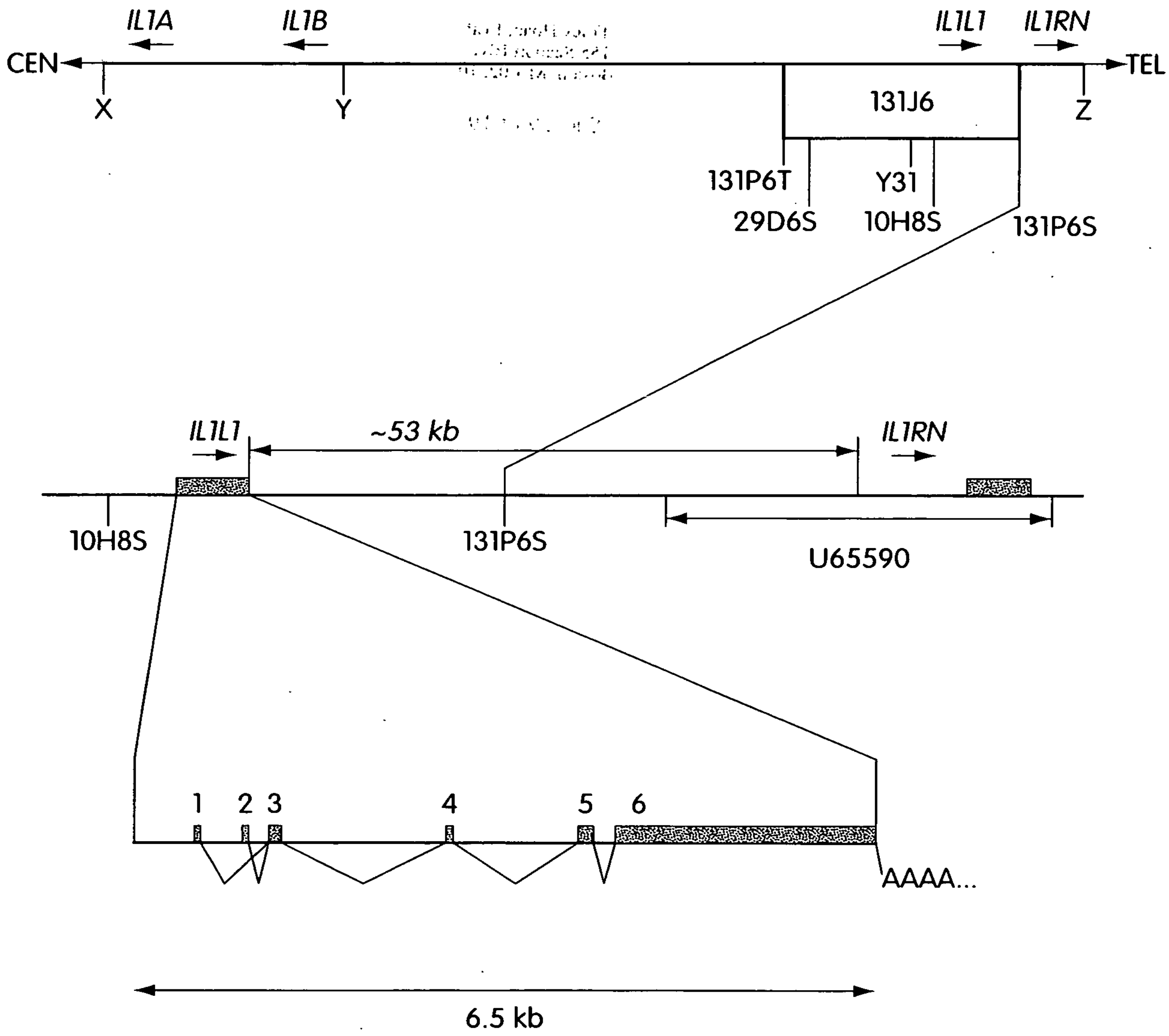
IL1A
IL1B
IL1L1
IL1RN
CEN
TEL
X
Y
Z
131J6
131P6T
29D6S
Y31
10H8S
131P6S
IL1L1
~53 kb
IL1RN
10H8S
131P6S
U65590
1
2
3
4
5
6
AAAA...
6.5 kb

Fig. 9

RECEIVED
SEP 19 2002
TECH CENTER 1600/2900

```
cDNA SEQUENCES CONTAINING EXON 1
CTGGCAATGGCAGGCAGGAAAGACAGAGGAAGGAAGGAGGGAGAAGGGAAGGAGTGAAGGAAGGAGTGAAAAA// exon 3
^                            ^
-74'   M  A  G  R  K  D  R  G  R  K  E  G  E  G  K  E ***          ***

cDNA SEQUENCES CONTAINING EXON 2
TTGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAAAGGAACATTCTGAG// exon 3
^                             ^              ^     ^
-54                                          ^
```

Fig. 10A

5' flank	start	exon	start seq	cDNA	end seq	end	3'flank
	+ 451	1	CTGGCAATGG	-74'- -1'	AGTGAAAAAG	+ 524	gtaaggaaga
	+ 969	2	TTGGAGGAAC	-54 - -1	ACATTCTGAG	+1022	gtatgctctg
tccaaaatag	+1193	3	GGGAGTCTAC	1 - 56	TGTGCTTCCG	+1248	gtgagtgtat
gatgtttcag	+2631	4	AATGAAGGAC	57 - 142	GTCATTAAAG	+2716	gttggtgatg
tttcccacag	+3905	5	GTGAAGAGAT	143 - 270	AACACTAGAG	+4032	gtgagacttg
ctgccggcag	+4234	6	CCAGTGAACA	271 - 2559	AGAGAAAGAG	+6522	aaacaaatgc

Fig. 10B

```
IL-1L1   MVLSGALCFR(2)MKDSALKVLYLHNNQLLAGGLHAGKVIKG(1)EEISVVPNRWLDASLSP
IL-1ra ..RKSSKMQAFR(2)IWDVNQKTFYLRNNQLVAGYLQGPNVNLEE(1)KIDVVP-----IEPHA

IL-1L1   VILGVQGGSQCLSCG-VGQEPTLTLE(3)VNIMELYLGAKESKSFTFYRRDM..
IL-1ra   LFLGIHGGKMCLSCVKSGDETRLQLE(3)VNITDLSENRKQDKRFAFIRSDS..
```

Fig. 10C

RECEIVED
SEP 1 9 2002
TECH CENTER 1600/2900


```
   1 CATGAGCAAA GATGTTAATA CAAAGATGTT TGTCACAACA TGGTTTTCAA TAGCAAAAAA
  61 AGAGAGAAAA ATATATAAAA GACAAATAAC AGTGGATAGG TTTCAATAAA TAATGTTACA
 121 GTGATACAGT TAAATACTAT ACAGCTATTG AAGCATGTCA TTATTCATAT TTAGTATGGA
 181 AAGATATTTT GCTATTTTGC TACATGAAAA AATGAGGTTG GAAAAAGTAT AGGTTTTGTG
 241 AATCTGTTGT ATGAAAGCTG TCTATAGTTA CATGTGTATG TGTGTGGAGG AAAAAGTGTT
 301 GTCATTGGTT TTCTGATGAT GCACTCAGAA AAGACAAGTA TTCACATTTT TTCTTGTGGC
 361 TGATCTGGAT TTTCAGGTTT TTCTACAATG AACATGTAGG CTGAACATTC CCTAAGCAGG
 421 AGAGTCCCAC CTCTAACATC TCCTGTAGGC CTGGCAATGG CAGGCAGGAA AGACAGAGGA
 481 AGGAAGGAGG GAGAAGGGAA GGAGTGAAGG AAGGAGTGAA AAAGGTAAGG AAGAAAGGGA
 541 ATAGGGGAGG AAGGGAGGAA ATGGGAAGGG AAAGAAGGAA AGGAAGGAAA GAGGGAGGGA
 601 AGAAAGGAAG GGAAAAGGGA GGGAGTGAGT GAATGAAAGA TGGAAAGAAG GAAGAAAGGG
 661 AGGGAGGCAG GGAGGAAAGA AAGTTGCGCT TCCCTTGAGC TGCCATGGGC ACTGACTCTT
 721 AGGGTCTGAA AGCCCCTGAG ATGCAAAAGC CTAGTGCTCA CAAAGAGCTG GAAAGCCTCA
 781 AGGAAGTTCT TCAATATTTC TGGAAGGAAA CTGTCTCCAG AAGCTTCCCT CCCCACGACA
 841 GATAATGAGC AGCAAGTGCT TCTGGCGACT TAGGGTGATG TGAAATCACG CTGGGAATCC
 901 TGCTCCTCCT CAGGTCCTGG CAGTTTCAGG GCCCCTCCCT AGGCCTTACT TAAAAGGCTG
 961 AGGCATCCTT GGAGGAACAG GCAGACTCCA CAGCTCCCGC CAGGAGAAAG GAACATTCTG
1021 AGGTATGCTC TGGGGCGCTG GTGGTACCGG AGCTCTCTCC TGACCCCAGA CCCAGAATCT
```

Fig. 11

```
1081 GCTCCGTGGA GGCTGTTCAC ATGCTGGGGA GCTCGGTGCA GCTGCTTGCT CCCCAGACCC
1141 CAGCCAACTC AGCCTCTCTC TCCATGATTT TCTGTTGTTT ATTCCAAAAT AGGGGAGTCT
1201 ACACCCTGTG GAGCTCAAGA TGGTCCTGAG TGGGGCGCTG TGCTTCCGGT GAGTGTATGA
1261 GGCCCTGGTT TGGTGGTGTC CTCCGGAGGA AGTGAGTTCT GGATAGACCC GTTGTCCAGC
1321 TCTGAGCAGG AGGGAGGAAG GGAGGGGCTG CCATTGCAGC TGGGAAATTG TGACCAGCAC
1381 CTCATTGCTC TTAGAGTTTT CCCAGCCTTT TTCAAATAGG GGCAGGACTG GGGCAGGCCA
1441 TCTCACAAGG GGTCCCTGAT GCTGAGGGGG ACAAGTGAAC CTCCCAGTCT AGAGCTCCAG
1501 CCAAGTCTAT CCAAGGTGGG AACGGGGGCC AGGATCCCTG CTCAGAGCTC CGCCATTGTC
1561 CCCCATCACA GTGAATGGAT GTAAGCTCAC CCACTCTGTG CCCCTACCTC CCTGCTACTC
1621 TTTGGGGATA ATAATAAAAC AAAAACCATT ACCATCAGCC AGTCTGTCCA CCCACTGGCA
1681 TGTACCAAGC CAGACACTCT GCCGTGTTCT GGGCTTAACA ACAGAGGATG AGAGTGGTCC
1741 TTTCTCTCAG TCTAATAAAG CACTTCCCAC GATGTGTTCT ATGGGACTCG ATTAGAGGAG
1801 TCCCACAGAG GCATCCAGGA GATGCTTTAC ACAGTGGAGC TCTCTGATCA AGTAAATGCA
1861 GGGAATTCTG CTTTCTACAT CCTCTCATAA GAGAACCACA GCCCAGCTCA GCATATGAGT
1921 GACTGAGGTT TTCTGAAGTA AGGCAACTTG TTGAATCGTA TTTAGCTATG CATCGACCCA
1981 ATTTTTACAC TGCATCCTTT TCCCCCATAT AACTTTTGGA GAAACCCACT TTAGGATACA
2041 TCTTCCACCT CATAGGATGC CAGGAAATCA ACTGAGTTCA AAGATGAGAA ACAACTTTGA
2101 AAAGTTAAAT AAAAGAAATT TAAATTTAAA GAAACTCCTC ACTTAGTAAG GAATATATGA
2161 CCAAATAGAA ATACATGTAT CTTGAAGAAT TGAAGAATCA GGCTTTAACG TGGAAGAGGC
```

Fig. 11 (Continued)

RECEIVED
SEP 19 2002
TECH CENTER 1600/2900

2221 CTGGATGTTA TCCAACCCAT CATCTTAGTG TAGCAATGGG GAGGCTCAGG CCCAGAGTGG

2281 GCGAGAGAGT TGTCTCCTGC GACTCAGCAG CATTGGAGGC ATAGATGGGG CAAGAACCTA

2341 GGGCTCTGAC TCACCGTGCA GCTTCTCTTC CAACAGGAGA TGGGTTGGGG CAGAAAAGGT

2401 TGAATAGGGT GAAGGAGCAA ACCACAGACT CCAGTGGGAG ACTGTGGGGT CATCCTCCTT

2461 GTAGGGCATG AGCCCAGCAG GGCTGGGAGA CAAGGCTGTG CTGTTACTTC TGGCACAGTA

2521 GGAAGAAAGA GAGACAAAAT GCCTGAGATC AGGGGGTTCT CTGGATCCAG GGCATGCTGG

2581 AGTGTCCACC CTCCTCCTAA TGTAGTCCTC ACCCCTTCCT GATGTTTCAG AATGAAGGAC

2641 TCGGCATTGA AGGTGCTTTA TCTGCATAAT AACCAGCTTC TAGCTGGAGG GCTGCATGCA

2701 GGGAAGGTCA TTAAAGGTTG GTGATGAAAC ATGACCCACT TTCCTTGGTC TCTATACACT

2761 CTCAGGGGAG GGGGCCTGAA GAGGGCTTAG AATAGTCATA CAGATTAGCA TAGGCCTACA

2821 GAGCCCAGGC ATTAGGGCAG CACAAACCAG GCTCTAAGCA AAGGCAAATA AAATACTACA

2881 CCTCTCAGCA AAGTGAAGAC ACACGCTCTG GGGCCACCTG AAGCTTCTGT GCAGAAGTGA

2941 GAATGTTTTC CAAGAGGCTT GTCTTGTCAT TCCCTTACAG GTAGATTTAG GTCAAGCATT

3001 GCATTCCCTG GGAGCCAGTA AGTACCAAGG AGAGAACTAA CGTAGATTCT CTATACCTTT

3061 TTTCCCATAT GGGAGTGGGT TTCTGCCTCT CCACCCTGGG TCCCCTCTGC TCTCTGAAGA

3121 TCCTCAGTCA CTTAGAGTGG AGGGACCCAG AGAACAGGTG GCATTGTTGG ACCTCCTGCT

3181 TGCTCACTCT GCCCCATGCA CTGCAACAGG TCCCTCTCTA AAATAGTTTG CACCTGCCCA

3241 CCTGGGGCAC CCTTGCTGAG CACAGATGCC AGGTAGATCC TTCAGCTAGG CCATATGTGT

3301 ATGTGTGTGC TTACTGGTGT ATGTATGTGT GCATGCAGGC ATATATGTGT GAGCATATGT

Fig. 11 (Continued)

3361 GTGCATGCAT GTATCTGTAT GTAACCATGT ATGTGTGAGT GCAGGTATGT AGGTATGAGC

3421 ATGTGTGTGT ATATGTATAT GTGTGCATGC ATGTATCTGT GCATGTATGT ATCTGATGTA

3481 TGTGGGTGGT GAGGGGATGT ACAGAGAGGA ATGAGACCCT CTTTTGCTCT CAGCAACCTC

3541 ACAGGGTGTA GAAAGTTGTC CAAACAATTC CAAAGGGGGG CTTATTAAGA CAGGGTTCAG

3601 AAAAAGGCCT GAGACCCAAG GGGCATTAAA GGAGGGGGTT GAGTCTATTT TGGGTTGTAG

3661 AGGCTTGAAG ATTTGACCCT GAACTAGAGG GTGGAGTGGA GGTGGTACAA TGTGCTTCCA

3721 TGCCTTGATG TCCACTCTGG GCCAGTGGAC AGGAGAAGCC ATGTCATGAC AGCTGCTGAG

3781 AAGCCTCCCT TCTGCCCAGC CTGGGGGCAG GCCGTCTCAC AGCAGTCCTG TGCCCTAGAG

3841 CCCAGGACAG GGGAAGAAGG AGGGAAAGGC ATCCAGGGCC CTGCATCTGG CCTCTTTCCC

3901 ACAGGTGAAG AGATCAGCGT GGTCCCCAAT CGGTGGCTGG ATGCCAGCCT GTCCCCCGTC

3961 ATCCTGGGTG TCCAGGGTGG AAGCCAGTGC CTGTCATGTG GGGTGGGGCA GGAGCCGACT

4021 CTAACACTAG AGGTGAGACT TGGGGCATCC TCACTGGGGA CTCAGCCACA GATGCTGAGC

4081 CTACTGAAGC CGGGCAGCCC ACAGCCCTGG TGCTGTGGGA CACCCTAGCA GGATTCTGTT

4141 GATGGCAGCT TTGCCTCCTC CCTAAGGATC CTGCCCAGCC CTCCCTCTGC CCCTGCTTCT

4201 GCCCTCACCT GACCTCCCCT CCTCTGCCGG CAGCCAGTGA ACATCATGGA GCTCTATCTT

4261 GGTGCCAAGG AATCCAAGAG CTTCACCTTC TACCGGCGGG ACATGGGGCT CACCTCCAGC

4321 TTCGAGTCGG CTGCCTACCC GGGCTGGTTC CTGTGCACGG TGCCTGAAGC CGATCAGCCT

4381 GTCAGACTCA CCCAGCTTCC CGAGAATGGT GGCTGGAATG CCCCCATCAC AGACTTCTAC

4441 TTCCAGCAGT GTGACTAGGG CAACGTGCCC CCCAGAACTC CCTGGGCAGA GCCAGCTCGG

Fig. 11 (Continued)

4501 GTGAGGGGTG AGTGGAGGAG ACCCATGGCG GACAATCACT CTCTCTGCTC TCAGGACCCC

4561 CACGTCTGAC TTAGTGGGCA CCTGACCACT TTGTCTTCTG GTTCCCAGTT TGGATAAATT

4621 CTGAGATTTG GAGCTCAGTC CACGGTCCTC CCCCACTGGA TGGTGCTACT GCTGTGGAAC

4681 CTTGTAAAAA CCATGTGGGG TAAACTGGGA ATAACATGAA AAGATTTCTG TGGGGGTGGG

4741 GTGGGGGAGT GGTGGGAATC ATTCCTGCTT AATGGTAACT GACAAGTGTT ACCCTGAGCC

4801 CCGCAGGCCA ACCCATCCCC AGTTGAGCCT TATAGGGTCA GTAGCTCTCC ACATGAAGTC

4861 CTGTCACTCA CCACTGTGCA GGAGAGGGAG GTGGTCATAG AGTCAGGGAT CTATGGCCCT

4921 TGGCCCAGCC CCACCCCCTT CCCTTTAATC CTGCCACTGT CATATGCTAC CTTTCCTATC

4981 TCTTCCCTCA TCATCTTGTT GTGGGCATGA GGAGGTGGTG ATGTCAGAAG AAATGGCTCG

5041 AGCTCAGAAG ATAAAAGATA AGTAGGGTAT GCTGATCCTC TTTTAAAAAC CCAAGATACA

5101 ATCAAAATCC CAGATGCTGG TCTCTATTCC CATGAAAAAG TGCTCATGAC ATATTGAGAA

5161 GACCTACTTA CAAAGTGGCA TATATTGCAA TTTATTTTAA TTAAAAGATA CCTATTTATA

5221 TATTTCTTTA TAGAAAAAAG TCTGGAAGAG TTTACTTCAA TTGTAGCAAT GTCAGGGTGG

5281 TGGCAGTATA GGTGATTTTT CTTTTAATTC TGTTAATTTA TCTGTATTTC CTAATTTTTC

5341 TACAATGAAG ATGAATTCCT TGTATAAAAA TAAGAAAAGA AATTAATCTT GAGGTAAGCA

5401 GAGCAGACAT CATCTCTGAT TGTCCTCAGC CTCCACTTCC CCAGAGTAAA TTCAAATTGA

5461 ATCGAGCTCT GCTGCTCTGG TTGGTTGTAG TAGTGATCAG GAAACAGATC TCAGCAAAGC

5521 CACTGAGGAG GAGGCTGTGA TGAGTTTGTG TGGCTGGAAT CTCTGGGTAA GGAACTTAAA

5581 GAACAAAAAT CATCTGGTAA TTCTTTCCTA GAAGGATCAC AGCCCCTGGG ATTCCAAGGC

Fig. 11 (Continued)

5641 ATTGGATCCA GTCTCTAAGA AGGCTGCTGT ACTGGTTGAA TTGTGTCCCC CTCAAATTCA

5701 CATCCTTCTT GGAATCTCAG TCTGTGAGTT TATTTGGAGA TAAGGTCTCT GCAGATGTAG

5761 TTAGTTAAGA CAAGGTCATG CTGGATGAAG GTAGACCTAA ATTCAATATG ACTGGTTTCC

5821 TTGTATGAAA AGGAGAGGAC ACAGAGACAG AGGAGACGCG GGGAAGACTA TGTAAAGATG

5881 AAGGCAGAGA TCGGAGTTTT GCAGCCACAA GCTAAGAAAC ACCAAGGATT GTGGCAACCA

5941 TCAGAAGCTT GGAAGAGGCA AAGAAGAATT CTTCCCTAGA GGCTTTAGAG GGATAACGGC

6001 TCTGCTGAAA CCTTAATCTC AGACTTCCAG CCTCCTGAAC GAAGAAAGAA TAAATTTCGG

6061 CTGTTTTAAG CCACCAAGGA TAATTGGTTA TGGCAGCTCT AGGAAACTAA TACAGCTGCT

6121 AAAATGATCC CTGTCTCCTC GTGTTTACAT TCTGTGTGTG TCCCCTCCCA CAATGTACCA

6181 AAGTTGTCTT TGTGACCAAT AGAATATGGC AGAAGTGATG GCATGCCACT TCCAAGATTA

6241 GGTTATAAAA GACACTGCAG CTTCTACTTG AGCCCTCTCT CTCTGCCACC CACCGCCCCC

6301 AATCTATCTT GGCTCACTCG CTCTGGGGGA AGCTAGCTTC CATGCTATGA GCAGGCCTAT

6361 AAAGAGACTT ATGTGGTAAA AAATGAAGTC TCCTGCCCAC AGCCACATTA GTGAACCTAG

6421 AAGCAGAGAC TCTGTGAGAT AATCAATGTT TGTTGTTTTA AGTTGCTCAG TTTTGGTCTA

6481 ACTTGTTATG CAGCAATAGA TAAATAATAT GCAGAGAAAG AGAAACAAAT GCATTTGTTT

Fig. 11 (Continued)

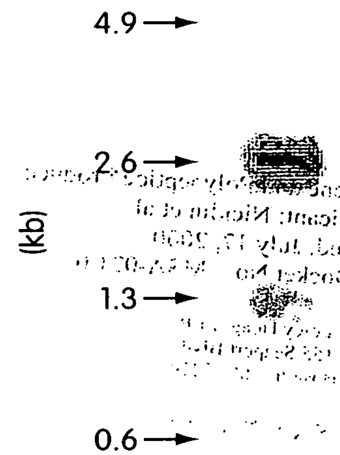

Fig. 12A

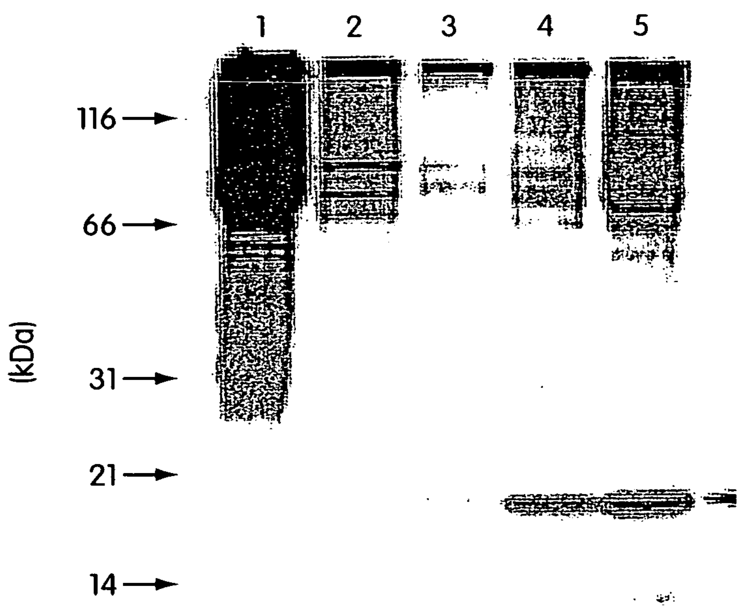

Fig. 12B

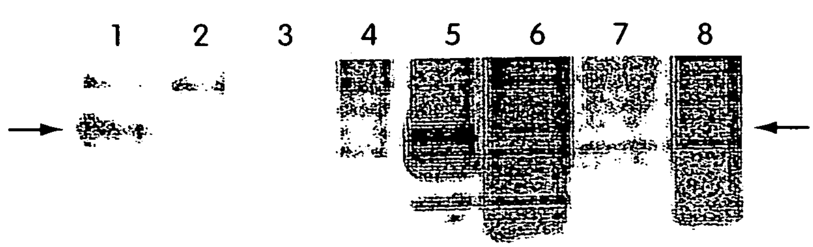

Fig. 12C

```
                              Sheet 1  Sheet 2  Sheet3          Sheet 4
                          *  ** ** **      **     ***    *     * *    **
                             >>>>>>>>  >>>>>    >>>>>          >>>>>>>
hIL-1L1                  MVLSGALCFRMKDSALKVLYLH NNQLLAG GLHAGKVIKGEEISVVP  46
mIL-1L1                  MVLSGALCFRMKDSALKVLYLH NNQLLAG GLHAFKVIKGEEISVVP  46
hIL-1ra            RPSGRKSSKMQAFRIWDVNQKTFYLR NNQLVAG YLQGPNVNLEEKIDVVP  50
hIL-1beta              APVRSLNCTLRDSQQKSLVMSGPYELKAL HLQGQDMEQQVVFSMSF  46
hIL-1alpha  SAPFSFLSNVKYNFMRIIKYEFILNDALNQSIIRANDQYLTAAALHNLDEAV KFDMGAY  59
hIL-18           YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAP RTIFIISMY  52

               Sheet 5    Sheet 6     Sheet 7                  Sheet 8
          *   * ******    * *  * * ** *********                  **
                >>>>>     >>>>>> >  >>>>>>>>                   >>>>>
hIL-1L1     NRWLDASLSPVILGVQG GSQCLSCG VGQEPTLTLEPVNIMELYLGAKESKSFTFYRR 103
mIL-1L1     NRALDASLSPVILGVQG GSQCLSCG TEKGPILKLEPVNIMELYLGAKESKSFTFYRR 103
hIL-1ra          IEPHALFLGIHG GKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRS 103
hIL-1beta   VQGEESNDKIPVALGLK EKNLYLSCVLKDDKPTLQLESVDPKNYPK KKMEKRFVFNKI 104
hIL-1alpha  KSSKDDAKITVILRIS KTQLYVTAQ DEDQPVLLKEMPEIPKTIT  GSETNLLFFWE 114
hIL-18      KDSQ PRGMAVTISVKCEKISTLSCE   NKIISFKEMNPPDNIKDTKSDIIFFQRSVP 107

             Sheet 9    Sheet 10  Sheet 11           Sheet 12
          *  * * *   * * *  ***   *  ******       * *** **
         >>> >>>>>>>   >>>>>>     >>>>>>>           >>>>>>
hIL-1L1     DMGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD     155
mIL-1L1     DMGLTSSFESAAYPGWFLCTSPEADQPVRLTQIPEDPAWDAPITDFYFQQCD     155
hIL-1ra     DSGPTTSFESAACPGWFLCTAMEADQPVSLTNMPDEG  VMVTKFYFQEDE     152
hIL-1beta   EINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQ   DITDFTMQFVSS     153
hIL-1alpha  THGTKNYFTSVAHPNLFIAT  KQDYWVCLAGGP P     SITDFQILENQA     159
hIL-18      GHDNKMQFESSSYEGYFLACEKERDLFKLILKKEDELG  DRSIMFTVQNED     157
```

Fig. 13